

1/10

10	30	50
GGCACGAGGGGAAACTCTATTTTGAAAATGAATATATTTTGATTTAAACAATACAGAGAA		
70	90	110
GTCAAAATGGACACAATCTTCTTGTTGGAGTCTTCTATTGCTGTTTTTTGGAAAGTCAAGCC		
<u>M D T I F L W S L L L L F F G S Q A</u>		
130	150	170
TCAAGATGCTCAGCTCAAAAAAATACCGAATTTGCAGTGGATCTTTATCAAGAGGTTTCC		
S R C S A Q K N T E F A V D L Y Q E V S		
190	210	230
TTATCTCATAAGGACAACATTATATTTTCACCCCTTGAATAACTTTGGTTCTTGAGATG		
L S H K D N I I F S P L G I T L V L E M		
250	270	290
GTACAACTGGGAGCCAAAGGAAAAGCACAGCAGCAGATAAGACAAACTTTAAAACAACAG		
V Q L G A K G K A Q Q Q I R Q T L K Q Q		
310	330	350
GAAACCTCAGCTGGGGAAGAATTTTTGGTACTGAAGTCATTTTGCTCTGCCATCTCAGAG		
E T S A G E E F L V L K S F C S A I S E		
370	390	410
AAAAACAAGAATTTACATTTAATCTTGCCAATGCCCTCTACCTTCAAGAAGGATTCAC		
K K Q E F T F N L A N A L Y L Q E G F T		
430	450	470
GTGAAAGAACAGTATCTCCATGGCAACAAGGAATTTTTTCAGAGTGCTATAAACTGGTG		
V K E Q Y L H G N K E F F Q S A I K L V		
490	510	530
GATTTTCAAGATGCAAAGGCTTGTGCAGAGATGATAAGTACCTGGGTAGAAAGAAAAACA		
D F Q D A K A C A E M I S T W V E R K T		
550	570	590
GATGGAAAAATTAAAGACATGTTTTACAGGGGAAGAATTTGGCCCTCTGACTCGGCTTGTC		
D G K I K D M F S G E E F G P L T R L V		
610	630	650
CTGGTGAATGCTATTTATTTCAAAGGAGATTGAAACAGAAATTCAGAAAAGAGGACACA		
L V N A I Y F K G D W K Q K F R K E D T		
670	690	710
CAGCTGATAAATTTTACTAAGAAAAATGTTTCAACTGTCAAAATTCCAATGATGAAGGCT		
Q L I N F T K K N G S T V K I P M M K A		
730	750	770
CTTCTGAGAACAAAATATGGTTATTTTTCTGAATCTTCCCTGAACTACCAAGTTTTAGAA		
L L R T K Y G Y F S E S S L N Y Q V L E		
790	810	830
TTGTCTTACAAAGGTGATGAATTTAGCTTAATTATCATACTTCTGCAGAAGGTATGGAT		
L S Y K G D E F S L I I I L P A E G M D		
850	870	890

FIG. 1A

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ATAGAAGAAGTGGAAAACTAATTACTGCTCAACAAATCCTAAAAATGGCTCTCTGAGATG
I E E V E K L I T A Q Q I L K W L S E M
910 930 950
CAAGAAGAGGAAGTAGAAATAAGCCTCCCTAGATTTAAAGTAGAACAAAAAGTAGACTTC
Q E E E V E I S L P R F K V E Q K V D F
970 990 1010
AAAGACGTTTTGTATTCTTTGAACATAACCGAGATATTTAGTGGTGGCTGCGACCTTTCT
K D V L Y S L N I T E I F S G G C D L S
1030 1050 1070
GGAATAACAGATTCATCTGAAGTGTATGTTTCCCAAGTGACGCAAAAAGTTTTCTTTGAG
G I T D S S E V Y V S Q V T Q K V F F E
1090 1110 1130
ATAAATGAAGATGGTAGTGAAGCTGCAACATCAACTGGCATAACACATCCCTGTGATCATG
I N E D G S E A A T S T G I H I P V I M
1150 1170 1190
AGTCTGGCTCAAAGCCAATTTATAGCAAATCATCCATTTCTGTTTATTATGAAGCATAAT
S L A Q S Q F I A N H P F L F I M K H N
1210 1230 1250
CCAACAGAATCAATTCTGTTTATGGGAAGAGTGACAAATCCCTGACACCCAGGAGATAAA
P T E S I L F M G R V T N P *
1270 1290 1310
AGGAAGAGATTTAGATTCACTGTGAATGAAAAGCACAGCCTCAGAATAAAAGATGATTTTC
1330 1350 1370
TCAAAAATAA

FIG.1B

1	M	Q	M	S	P	A	L	T	C	L	V	L	G	L	A	L	V	F	G	E	G	S	A	V	H	H	P	P	S	Y	PAI-1-M16006		
1	M	E	-	-	-	-	-	-	-	-	-	-	D	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	PAI-2 M18082	
1	M	D	-	-	-	-	-	T	I	F	L	W	S	L	L	L	F	F	G	S	-	-	-	-	-	Q	A	S	R	-	C	HPASD50P protein	
31	V	A	H	L	A	S	D	F	G	V	R	V	F	Q	Q	V	A	Q	A	S	K	D	R	N	V	V	F	S	P	Y	PAI-1 M16006		
6	V	A	N	-	-	T	L	F	A	L	N	L	F	K	H	L	A	K	A	S	P	T	Q	N	L	F	L	S	P	W	PAI-2 M18082		
22	S	A	Q	K	N	I	E	F	A	V	D	L	Y	Q	E	V	S	L	S	H	K	D	-	N	I	I	F	S	P	L	HPASD50P protein		
61	G	V	A	S	V	L	A	M	L	Q	L	T	T	G	G	E	T	Q	Q	Q	I	Q	A	A	M	G	F	K	I	D	PAI-1 M16006		
34	S	I	S	S	T	M	A	M	V	Y	M	G	S	T	E	D	Q	M	A	K	V	L	Q	V	L	Q	F	N	E	V	PAI-2 M18082		
51	G	I	T	L	V	L	E	M	V	Q	L	G	A	K	G	K	A	Q	Q	Q	I	R	Q	T	L	-	-	K	Q	Q	HPASD50P protein		
91	D	K	G	M	A	P	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	PAI-1 16006	
64	G	A	N	A	V	T	P	M	T	P	E	N	F	T	S	C	G	F	M	Q	Q	I	Q	K	G	S	Y	P	D	A	PAI-2 M18082		
79	E	T	S	A	G	E	-	-	-	-	-	-	-	-	-	-	E	F	L	-	-	-	-	-	-	-	-	-	-	-	-	HPASD50P protein	
98	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	R	H	L	Y	K	E	L	M	G	P	W	N	K	D	E	I	PAI-1 M16006
94	I	L	Q	A	A	D	K	I	H	S	S	F	R	S	L	S	S	A	I	N	A	S	T	G	D	Y	L	L	L	L	PAI-2 M18082		
88	-	-	-	-	-	-	-	-	-	-	-	-	-	V	L	K	S	F	C	S	A	I	S	E	K	K	Q	E	F	T	F	HPASD50P protein	
115	S	T	T	D	A	I	F	V	Q	R	D	L	K	L	V	Q	G	F	M	P	H	F	F	R	L	F	R	S	T	V	PAI-1 M16006		
124	E	S	V	N	K	L	F	G	E	K	S	A	S	F	R	E	Y	I	R	L	C	Q	K	Y	Y	Y	S	S	E	P	PAI-2 M18082		
106	N	L	A	N	A	L	Y	L	Q	E	G	F	T	V	K	E	Q	Y	L	H	G	N	K	E	F	F	Q	S	A	I	HPASD50P protein		

FIG.2A

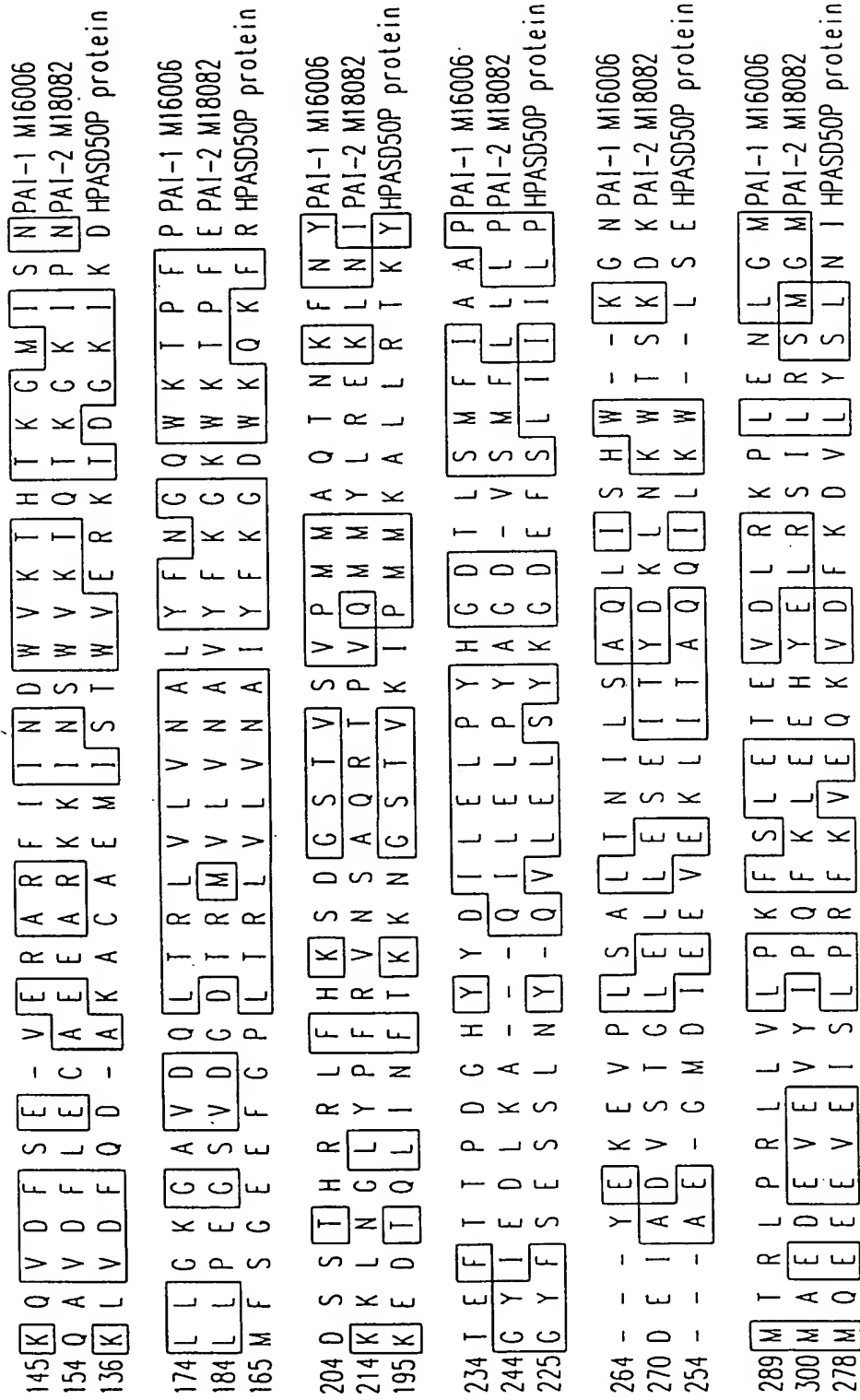


FIG.2B

319	T	D	M	F	R	Q	F	Q	A	D	F	I	S	L	S	D	Q	E	P	L	H	V	A	Q	A	L	Q	K	V	K	PAI-1	M16006
330	E	D	A	F	N	K	G	R	A	N	F	S	G	M	S	E	R	N	D	L	F	L	S	E	V	F	H	Q	A	M	PAI-2	M18082
308	T	E	I	F	S	G	-	G	C	D	L	S	G	I	T	D	S	S	E	V	Y	V	S	Q	V	T	Q	K	V	F	HPASD50P	protein
349	I	E	V	N	E	S	G	T	V	A	S	S	S	T	A	V	I	V	S	A	R	M	-	-	A	P	E	E	I	T	PAI-1	M16006
360	V	D	V	N	E	E	G	T	E	A	A	A	G	T	G	G	V	M	T	G	R	T	G	H	G	P	Q	F	V	PAI-2	M18082	
337	F	E	T	N	E	D	G	S	E	A	A	T	S	T	G	I	H	I	P	V	I	M	S	L	A	Q	S	Q	F	T	HPASD50P	protein
377	M	D	R	P	F	L	F	V	V	R	H	N	P	T	G	T	V	L	F	M	G	Q	V	M	E	-	P				PAI-1	M16006
390	A	D	H	P	F	L	F	L	I	M	H	K	I	T	K	C	I	L	F	F	G	R	F	C	S	P				PAI-2	M18082	
367	A	N	H	P	F	L	F	I	M	K	H	N	P	T	E	S	I	L	F	M	G	R	V	T	N	P					HPASD50P	protein

Decoration 'Decortion #1': Box residues that match the Consensus exactly.

FIG.2C

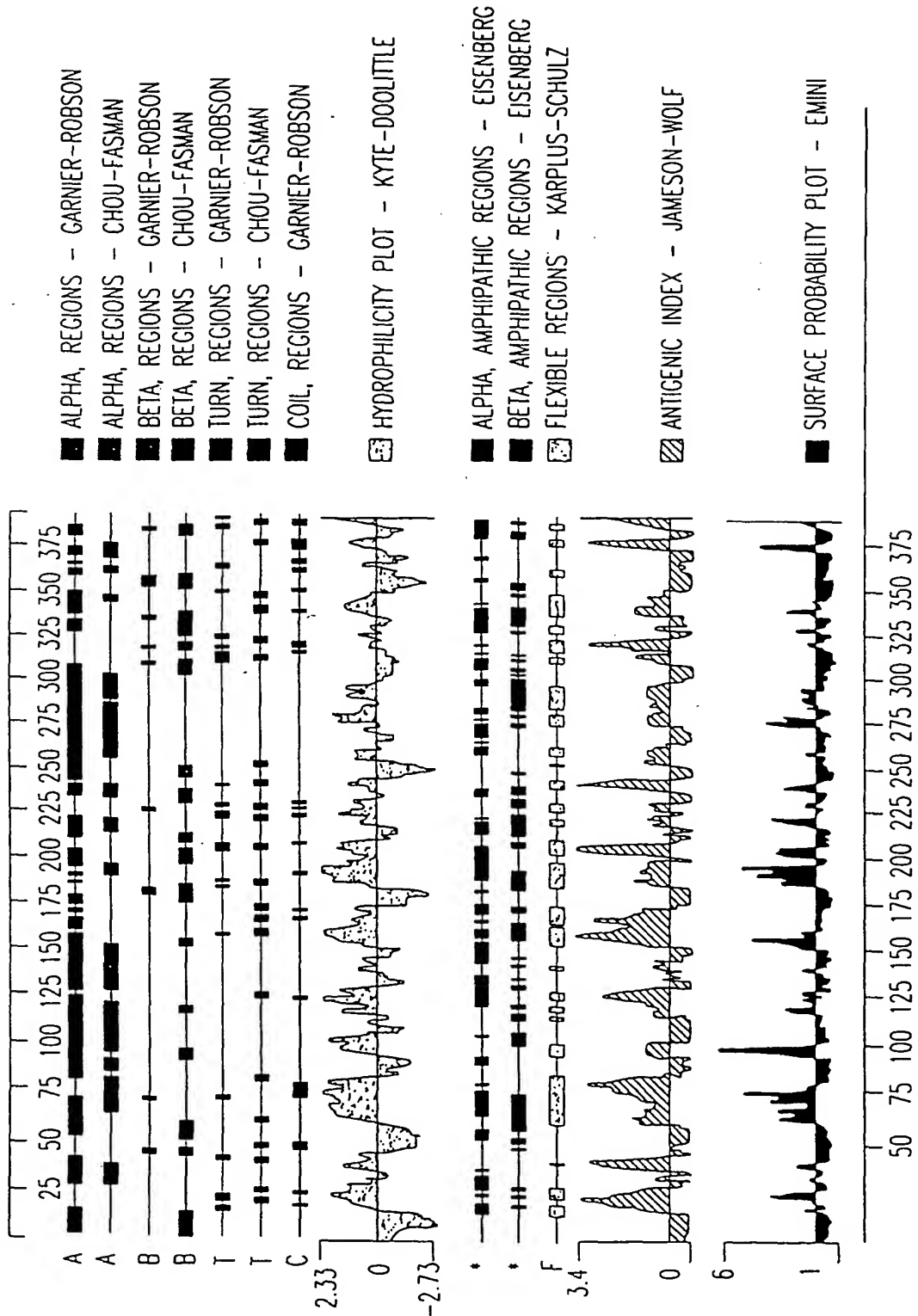


FIG.3

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GGCACGAGGGG	AAAACTCTAT	TTTGAAAATG	AATATATTTT	GATTTAAACA	ATACAGAGAA	60
GTCAAA	ATG GAC ACA ATC TTC TTG TGG AGT CTT CTA TTG CTG TTT	JTT	108			
Met Asp Thr Ile Phe Leu Trp Ser Leu Leu Leu Leu Phe Phe						
GCA AGT CAA GCC TCA AGA TGC TCA GCT CAA AAA AAT ACC GAA TTT GCA		156				
Gly Ser Gln Ala Ser Arg Cys Ser Ala Gln Lys Asn Thr Glu Phe Ala						
GTG GAT CTT TAT CAA GAG GTT TCC TTA TCT CAT AAG GAC AAC ATT ATA		204				
Val Asp Leu Tyr Gln Glu Val Ser Leu Ser His Lys Asp Asn Ile Ile						
TTT TCA CCC CTT GGA ATA ACT TTG GTT CTT GAG ATG GTA CAA CTG GGA		252				
Phe Ser Pro Leu Gly Ile Thr Leu Val Leu Glu Met Val Gln Leu Gly						
GCC AAA GGA AAA GCA CAG CAG CAG ATA AGA CAA ACT TTA AAA CAA CAG		300				
Ala Lys Gly Lys Ala Gln Gln Gln Ile Arg Gln Thr Leu Lys Gln Gln						
GAA ACC TCA GCT GGG GAA GAA TTT TTG GTA CTG AAG TCA TTT TGC TCT		348				
Glu Thr Ser Ala Gly Glu Glu Phe Leu Val Leu Lys Ser Phe Cys Ser						
GCC ATC TCA GAG AAA AAA CAA GAA TTT ACA TTT AAT CTT GCC AAT GCC		396				
Ala Ile Ser Glu Lys Lys Gln Glu Phe Thr Phe Asn Leu Ala Asn Ala						
CTC TAC CTT CAA GAA GGA TTC ACT GTG AAA GAA CAG TAT CTC CAT GGC		444				
Leu Tyr Leu Gln Glu Gly Phe Thr Val Lys Glu Gln Tyr Leu His Gly						
AAC AAG GAA TTT TTT CAG AGT GCT ATA AAA CTG GTG GAT TTT CAA GAT		492				
Asn Lys Glu Phe Phe Gln Ser Ala Ile Lys Leu Val Asp Phe Gln Asp						
GCA AAG GCT TGT GCA GAG ATG ATA AGT ACC TGG GTA GAA AGA AAA ACA		540				
Ala Lys Ala Cys Ala Glu Met Ile Ser Thr Trp Val Glu Arg Lys Thr						
GAT GGA AAA ATT AAA GAC ATG TTT TCA GGG GAA GAA TTT GGC CCT CTG		588				
Asp Gly Lys Ile Lys Asp Met Phe Ser Gly Glu Glu Phe Gly Pro Leu						
ACT CGG CTT GTC CTG GTG AAT GCT ATT TAT TTC AAA GGA GAT TGG AAA		636				
Thr Arg Leu Val Leu Val Asn Ala Ile Tyr Phe Lys Gly Asp Trp Lys						
CAG AAA TTC AGA AAA GAG GAC ACA CAG CTG ATA AAT TTT ACT AAG AAA		684				
Gln Lys Phe Arg Lys Glu Asp Thr Gln Leu Ile Asn Phe Thr Lys Lys						
AAT GGT TCA ACT GTC AAA ATT CCA ATG ATG AAG GCT CTT CTG AGA ACA		732				
Asn Gly Ser Thr Val Lys Ile Pro Met Met Lys Ala Leu Leu Arg Thr						
AAA TAT GGT TAT TTT TCT GAA TCT TCC CTG AAC TAC CAA GTT TTA GAA		780				
Lys Tyr Gly Tyr Phe Ser Glu Ser Ser Leu Asn Tyr Gln Val Leu Glu						
TTG TCT TAC AAA GGT GAT GAA TTT AGC TTA ATT ATC ATA CTT CCT GCA		828				
Leu Ser Tyr Lys Gly Asp Glu Phe Ser Leu Ile Ile Ile Leu Pro Ala						
GAA GGT ATG GAT ATA GAA GAA GTG GAA AAA CTA ATT ACT GCT CAA CAA		876				
Glu Gly Met Asp Ile Glu Glu Val Glu Lys Leu Ile Thr Ala Gln Gln						
ATC CTA AAA TGG CTC TCT GAG ATG CAA GAA GAG GAA GTA GAA ATA AGC		924				
Ile Leu Lys Trp Leu Ser Glu Met Gln Glu Glu Glu Val Glu Ile Ser						
CTC CCT AGA TTT AAA GTA GAA CAA AAA GTA GAC TTC AAA GAC GTT TTG		972				
Leu Pro Arg Phe Lys Val Glu Gln Lys Val Asp Phe Lys Asp Val Leu						
TAT TCT TTG AAC ATA ACC GAG ATA TTT AGT GGT GGC TGC GAC CTT TCT		1020				
Tyr Ser Leu Asn Ile Thr Glu Ile Phe Ser Gly Gly Cys Asp Leu Ser						
GCA ATA ACA GAT TCA TCT GAA GTG TAT GTT TCC CAA GTG ACG CAA AAA		1068				
Gly Ile Thr Asp Ser Ser Glu Val Tyr Val Ser Gln Val Thr Gln Lys						
GTT TTC TTT GAG ATA AAT GAA GAT GGT AGT GAA GCT GCA ACA TCA ACT		1116				
Val Phe Phe Glu Ile Asn Glu Asp Gly Ser Glu Ala Ala Thr Ser Thr						
GGC ATA CAC ATC CCT GTG ATC ATG AGT CTG GCT CAA AGC CAA TTT ATA		1164				

FIG.4A

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Gly Ile His Ile Pro Val Ile Met Ser Leu Ala Gln Ser Gln Phe Ile	
GCA AAT CAT CCA TTT CTG TTT ATT ATG AAG CAT AAT CCA ACA GAA TCA	1212
Ala Asn His Pro Phe Leu Phe Ile Met Lys His Asn Pro Thr Glu Ser	
ATT CTG TTT ATG GGA AGA GTG ACA AAT CCT GAC ACC CAG GAG ATA AAA	1260
Ile Leu Phe Met Gly Arg Val Thr Asn Pro Asp Thr Gln Glu Ile Lys	
GGA AGA GAT TTA GAT TCA CTG TGAATGAAAA GCACAGCCTC AGAATAAAAG	1311
Gly Arg Asp Leu Asp Ser Leu	
ATGATTTCTC AAAAATAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1370

FIG.4B

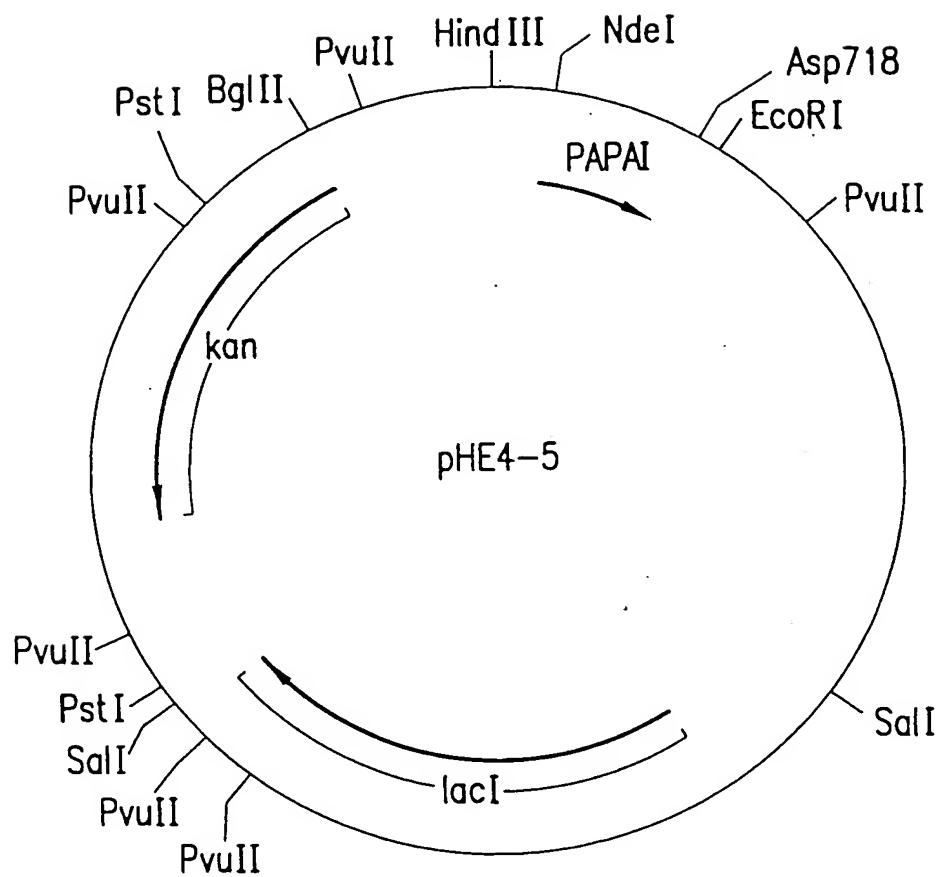


FIG.5

1 AAGCTTAAAAAACTGCAAAAAATAGT ⁻³⁵ OPERATOR1 TTGACTTGTGAGCGGATAACAA

50 ⁻¹⁰ TAAGATGTACCCAA ^{OPERATOR2} TTTGTGAGCGCGGATAACAA TTTCACACATTAA

94 ^{S/D} ACAGCAGAAATTA CATATG

FIG.6